GGGCCTAGGG CGCCGGGTCA GGGGCCTCGA GATCGGGCTT GGGCCCAGAG C ATG TTC 57
Met Phe
1

CAG ATC CCA GAG TTT GAG CCG AGT GAG CAG GAA GAC TCC AGC TCT GCA 105
Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser Ser Ala
5 10 15

GAG AGG GGC CTG GGC CCC AGC CCC GCA GGG GAC GGG CCC TCA GGC TCC 153
Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser Gly Ser
20 25 30

GGC AAG CAT CAT CGC CAG GCC CCA GGC CTC CTG TGG GAC GCC AGT CAC 201
Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala Ser His
35 40 45 50

CAG CAG GAG CAG CCA ACC AGC AGC AGC CAT CAT GGA GGC GCT GGG GCT 249
Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala Gly Ala
55 60 65

GTG GAG ATC CGG AGT CGC CAC AGC TCC TAC CCC GCG GGG ACG GAG GAC 297
Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr Glu Asp
70 75 80

GAC GAA GGG ATG GGG GAG GAG CCC AGC CCC TTT CGG GGC CGC TCG CGC 345
Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg Ser Arg
85 90 95

TCG GCG CCC CCC AAC CTC TGG GCA GCA CAG CGC TAT GGC CGC GAG CTC 393
Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu
100 105 110

CGG AGG ATG AGT GAC GAG TTT GTG GAC TCC TTT AAG AAG GGA CTT CCT 441
Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly Leu Pro
115 120 125 130

CGC CCG AAG AGC GCG GGC ACA GCA ACG CAG ATG CGG CAA AGC TCC AGC 489
Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser Ser Ser
135 140 145

TGG ACG CGA GTC TTC CAG TCC TGG TGG GAT CGG AAC TTG GGC AGG GGA 537
Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly Arg Gly
150 155 160

Fig. 1A

AGC TCC GCC CCC TCC CAG TGACCTTCGG TCCACATCCC GAAATCCACC 585
Ser Ser Ala Pro Ser Gln
165

CGTTCCCATT GCCCTGGGCA GCCATTTTGA ATATGGGAGG AAGTAAGTTC CCTCAGGCCT 645

ATGCAAAAAG AGGATCCGTG CTGTATCCTT TGGAGGGAGG GTTGACCCAG ATTCCCTTCC 705

GGTGTGTGTG AAGCCACGGA AGGTTGGTCC CATCGGAAGT TTTGGGTTTT CCGCCCACAG 765

CCGCCGGAAG TGGCTCCGTG GCCCCGCCCT CAGGTTCCGG GGTTTCCCCC AGGCGCCTGC 825

GCTAAGTAGC GAGCCAGGTT TAACCGTTGT GTCACCGGGA CCCGAGCCCC CGCGATGCCC 885

TGGGGGCCGT GATCAGTACC AAATGTTAAT AAAGCCCGCG TGTGTGCCAA AAAAAAAAA 945

A 946

Fig. 1B

ALIGNMENT OF MOUSE AND HUMAN BAD PROTEIN SEQUEUNCES

```
                    10        20        30        40
1   MGTPKQPSLAPAHALGLRKSDPGIRSLGSDAGGRRWRPAA   PmBad
1   ----------------------------------------   PBM1

                    50        60        70        80
41  QSMFQIPEFEPSEQEDASATDRGLGPSLTEDQPGPY----   PmBad
1   --MFQIPEFEPSEQEDSSSAERGLGPSPAGDGPSGSGKHH   PBM1

                    90        100       110       120
77  -LAPGLLGSNIHQQGRAATNSHHGGAGAMETRSRHSSYPA   PmBad
39  RQAPGLLWDASHQQEQPTSSSHHGGAGAVEIRSRHSSYPA   PBM1

                    130       140       150       160
116 GTEEDEGMEEELSPFRGRSRSAPPNLWAAQRYGRELRRMT   PmBad
79  GTEDDEGMGEEPSPFRGRSRSAPPNLWAAQRYGRELRRMS   PBM1

                    170       180       190       200
156 DEFEGSFK-GLPRPKSAGTATQMRQSAGWTRIIQSWWDRN   PmBad
119 DEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRN   PBM1

                    210
195 LGKGGSTPSQ                                 PmBad
159 LGRGSSAPSQ                                 PBM1
```

PmBad = mouse protein sequence
PBM1 = human protein sequence

Fig. 2

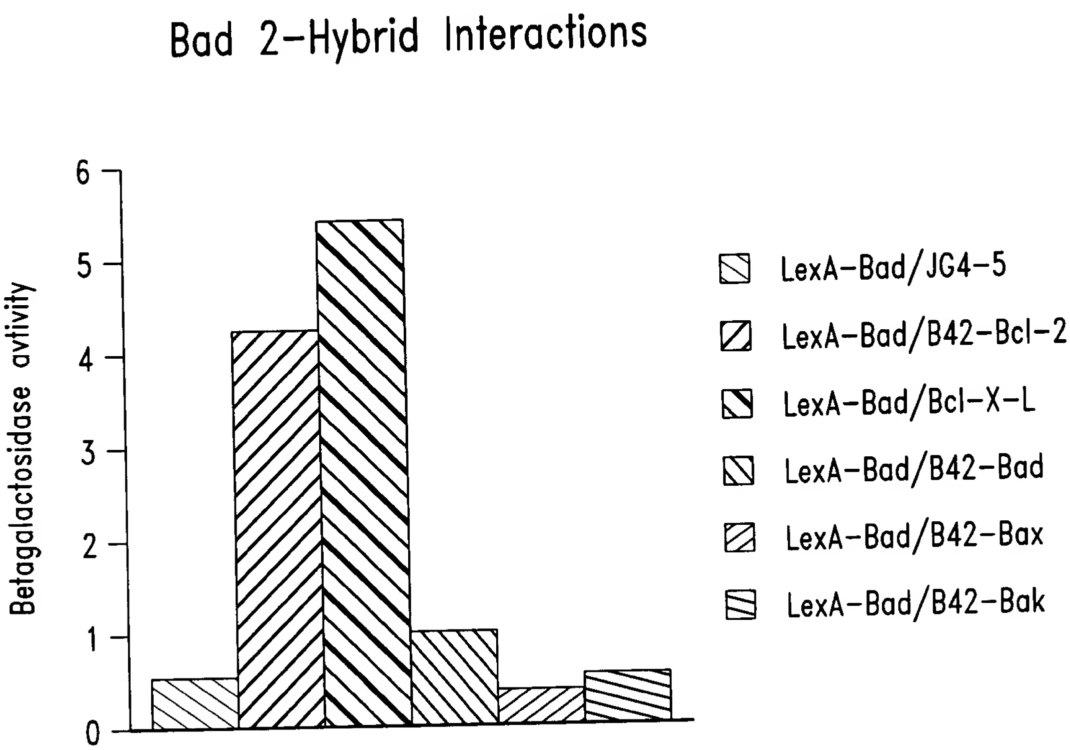
Bad 2-Hybrid Interactions
Betagalactosidase avtivity
0
1
2
3
4
5
6
LexA-Bad/JG4-5
LexA-Bad/B42-Bcl-2
LexA-Bad/Bcl-X-L
LexA-Bad/B42-Bad
LexA-Bad/B42-Bax
LexA-Bad/B42-Bak

Fig. 3

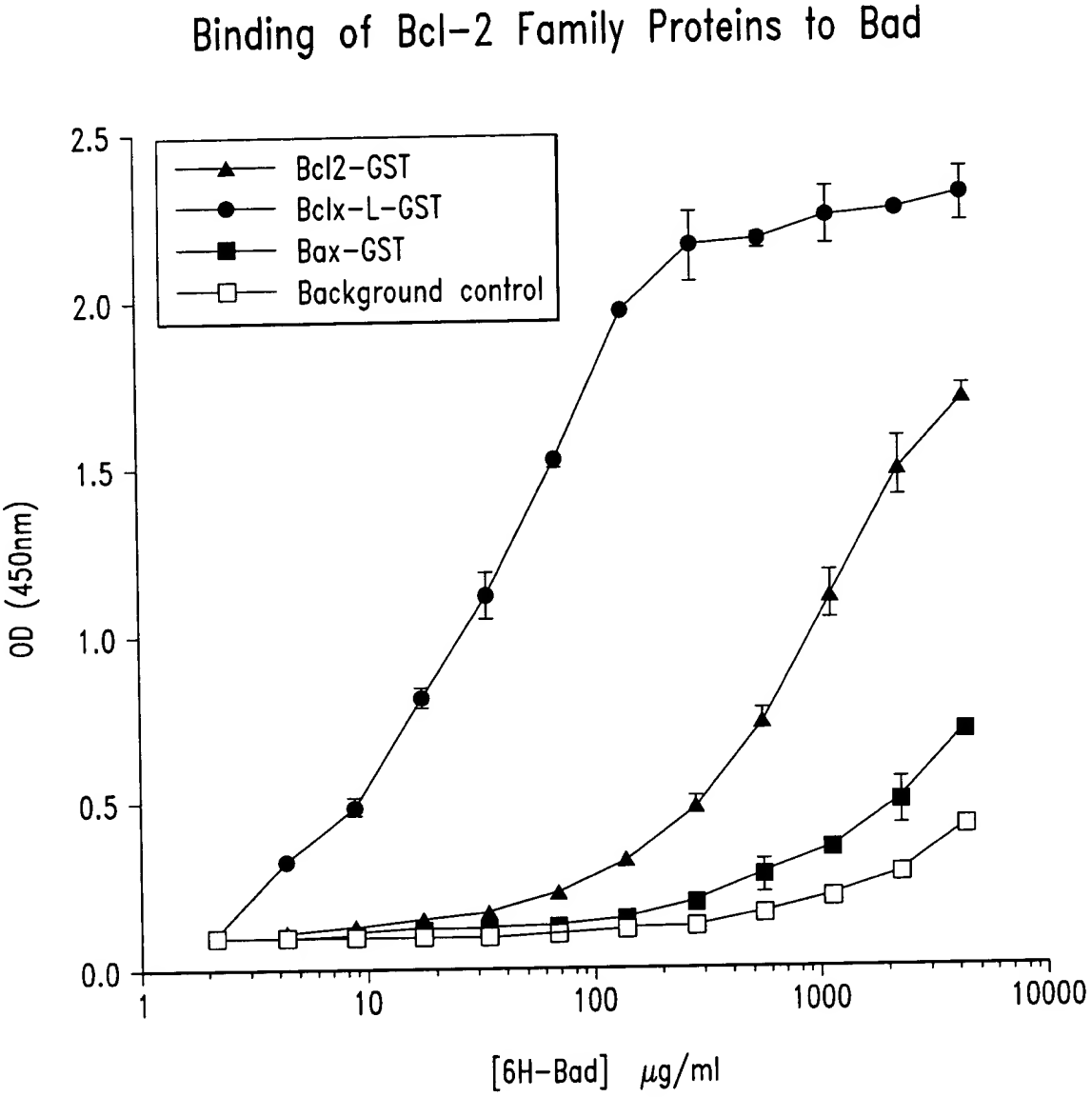
Binding of Bcl-2 Family Proteins to Bad
Bcl2-GST
Bclx-L-GST
Bax-GST
Background control
OD (450nm)
2.5
2.0
1.5
1.0
0.5
0.0
1
10
100
1000
10000
[6H-Bad] µg/ml

Fig. 4